cyno3-16 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC
TCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC
ACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTAGACGTGAGCCAG
GAAGACCCCGATGTCAAGTTCAACTGGTACGTAAATGGCGCGGAGGTGCATCATGCCCAGACGAAG
CCACGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAGGAC
TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA
ACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAG
GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC
GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCC
GACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT
CCGGGTAAA   (SEQ ID NO. 1)

cyno3-16 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGSLTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSQEDPDVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD
WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV
VEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
ʻPGK   (SEQ ID NO. 2)

FIG. 1

cyno33 genomic nucleotide sequence

```
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTTCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCACATCCCAGT
AACTCCCAATCTTCTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC
AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG
CCCTCCCGGCCCCCAAAGCAGAAAACTGTCTCCAAAACCAAAGGTGGGACCCGCGGGGCACGAGGGC
CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGCG
AGCAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTAC
TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA
(SEQ ID NO. 3)
```

cyno33 amino acid sequence

```
ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNG
QPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK
(SEQ ID NO. 4)
```

FIG. 2

cyno2-4 genomic nucleotide sequence

```
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACTGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAGGGGGAGTGTCTGCTG
GAAGCCATGCTCGGCCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC
TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCTCTGCACA
CATAGGGGCTGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCTCCTGACCT
AAGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG
TAACTCCCAATCTTCTCTCTGCAGAGTTCACACCCCCATGCCCACCATGCCCAGGTAAGCCAGCCC
AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCAGGGACAGGCCC
CGCCTGGGTGCTGACATGCCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATCATGCCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC
CTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC
CTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGCCA
CGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC
TACAGGGCAGCCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA
CCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG
CAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTACTT
CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGT
GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
(SEQ ID NO. 5)
```

cyno2-4 amino acid sequence

```
ASTKGPSVFPLASSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPREREQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ
PENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO. 6)
```

FIG. 3

cyno2-4cys genomic nucleotide sequence

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACTGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAGGGGGAGTGTCTGCTG
GAAGCCATGCTCGGCCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC
TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCTCTGCACA
CATAGGGGCTGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCTCCTGACCT
AAGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG
TAACTCCCAATCTTCTCTCTGCAGAGTTCACACCCCCATGCCCACCATGCCCAGGTAAGCCAGCCC
AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCAGGGACAGGCCC
CGCCTGGGTGCTGACATGCCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATCATGCCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC
CTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC
CTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGCCA
CGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC
TACAGGGCAGCCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA
CCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG
CAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTACTT
CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGT
GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA
(SEQ ID NO. 7)

cyno2-4cys amino acid sequence

ASTKGPSVFPLASCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ
PENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK
(SEQ ID NO. 8)

FIG. 4

cynods1 genomic nucleotide sequence

```
GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTCGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAGGGGGAGTGTCTGCTG
GAAGCCATGCTCGGCCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC
TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCTCTGCACA
CATAGGGGCTGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCTCCTGACCT
AAGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG
TAACTCCCAATCTTCTCTCTGCAGAGTTCACACCCCCATGCCCACCATGCCCAGGTAAGCCAGCCC
AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCAGGGACAGGCCC
CGCCTGGGTGCTGACATGCCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATCATGCCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC
CTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC
CTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGCCA
CGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC
TACAGGGCAGCCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA
CCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG
CAACGGGCAGCCGGAGAACAACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTACTT
CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGT
GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA
(SEQ ID NO. 9)
```

cynods1 amino acid sequence

```
ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ
PENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK
(SEQ ID NO. 10)
```

FIG. 5

cyno439 cDNA nucleotide sequence

CGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCCTGCTCCAGGAGCACCTC
CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTG
GAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTA
CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGT
CGTTCATGAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTTCACACGCCCATGTGATGACAC
AACTCCCCCATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCGTCTTCCC
CCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGT
GAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCCA
GACGAAGCCGCGGGAGAGGCAGTTCAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCA
CCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCAT
CCAGAAAACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTC
CCGGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGA
CATCGTCGTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACGCCGCCCGTGCT
GGACTCCGACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTC
CCTGTCTCCGGGTAAATGAGTCGACATGC   (SEQ ID NO. 11)

cyno439 amino acid sequence

VSSASTKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
SLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTRPCDDTTPPCPPCPAPELLGGPSVFVFP
PKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAQTKPRERQFNSTYRVVSVLTVTH
QDWLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSD
IVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK   (SEQ ID NO. 12)

FIG. 6

cyno686 cDNA nucleotide sequence

```
CGTCTCTAGTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCCTGCTCCAGGAGCACCTCCGAG
AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAAC
TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCC
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTT
CATGAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTTCACACGCCCATGTGATGACACAACT
CCCCCATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCGTCTTCCCCCCA
AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC
CAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGCGGAGGTGCATCATGCCCAGACG
AAGCCACGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAG
GACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAG
AAAACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGG
GAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATC
GTCGTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACGCCGCCCGTGCTGGAC
TCCGACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTG
TCTCCGGGTAAATGAGTCGACATGC        (SEQ ID NO. 13)
```

cyno686 amino acid sequence

```
RL*STKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTRPCDDTTPPCPPCPAPELLGGPSVFVFPP
KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQ
DWLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDI
VVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK     (SEQ ID NO. 14)
```

FIG. 7

cyno35 genomic nucleotide sequence

```
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTTCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCACATCCCAGT
AACTCCCAATCTTCTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC
AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG
CCCTCCCGGCCCCAAAGCAGAAAACTGTCTCCAAAACCAAAGGTGGGACCCGCGGGGCACGAGGGC
CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGAG
AGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTAC
TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA
(SEQ ID NO. 15)
```

cyno35 amino acid sequence

```
ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWESSG
QPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK*
(SEQ ID NO. 16)
```

FIG. 8

cyno36 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCACATCCCAGT
AACTCCCAATCTTCTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC
AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG
CCCTCCCGGCCCCAAAGCAGAAAACTGTCTCCAAAACCAAAGGTGGGACCCGCGGGGCACGAGGGC
CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGCG
AGCAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTAC
TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA
(SEQ ID NO. 17)

cyno36 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNG
QPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK*
(SEQ ID NO. 18)

FIG. 9

cyno477 cDNA nucleotide sequence

TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACAGCG
GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGCGCC
CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGCAGC
GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAGCCC
AGCAACACCAAGGTGGACAAGACAGTTGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGCT
GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCC
CGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAAC
TGGTACGTGGACGGCGTGGAGGTGCACAATGCCCAGACAAAGCCGCGGGAGGAGCAGTTCAACAGC
ACGTATCGCGTGGTCAGCGTCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACG
TGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCAAGGCAGAAAACTGTCTCCAAAACCAAAGGGCAG
CCCCGAGAGCCGCAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAGAACCAGGTCAGC
CTGACCTGCCTGATCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGCGAGCAACGGGCAG
CCGGAGAACACCTACAAGACCACGCCGCCCGTGCTGGACTCCGACGGCTCCTACTTCCTCTACAGC
AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   (SEQ ID
NO. 19).

cyno477 amino acid sequence

STKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS
VVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKALPAPRQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLIKGFYPSDIVVEWASNGQ
PENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSLSPGK*
(SEQ ID NO. 20)

FIG. 10

cyno32 genomic nucleotide sequence

```
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGGAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGGCCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCACATCCCAGT
AACTCCCAATCTTCTCTCTGCAGGGCTCCCATGTCGTTCCACGTGCCCACCGTGCCCAGGTAAGCC
AGCCCAGGCCTCACCCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG
GCCTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGC
CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCGCAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAG
AGCAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTAC
TTCCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA
(SEQ ID NO. 21)
```

cyno32 amino acid sequence

```
ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNG
QPENTYKTTPPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK*
(SEQ ID NO. 22)
```

FIG. 11

cyno3-18 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC
TCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAACATGTGGTGGTGGCAGCAAACCTCCCACG
TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC
AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTAGACGTGAGCCAGGAA
GACCCCGATGTCAAGTTCAACTGGTACGTAAATGGCGCGGAGGTGCATCATGCCCAGACGAAGCCA
CGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAGGACTGG
CTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAAACC
ATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAGGAG
CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTG
GAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGAC
GGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCG
GGTAAA   (SEQ ID NO. 23)

cyno3-18 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGSLTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEITCGGGSKPPTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSQEDPDVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDW
LNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVV
EWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK   (SEQ ID NO. 24)

FIG. 12

cyno1-3 cDNA nucleotide sequence

```
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC
ACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAG
GAAGACCCCGAGGTCCAGTTCAACTGGTACGTAAACGGCGCGGAGGTGCATCATGCCCAGACGAAG
CCACGGGAGACGCAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCGTCACACACCAGGAC
TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA
ACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAG
GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC
GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACAACTACAAGACCACCCCGCCCGTGCTGGACTCC
GACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT
CCGGGTAAA     (SEQ ID NO. 25)
```

cyno1-3 amino acid sequence

```
ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD
WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV
VEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK     (SEQ ID NO. 26)
```

FIG. 13

cyno1-4 cDNA nucleotide sequence

```
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC
ACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAG
GAAGACCCCGAGGTCCAGTTCAACTGGTACGTAAACGGCGCGGAGGTGCATCATGCCCAGACGAAG
CCACGGGAGACGCAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCGTCACACACCAGGAC
TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA
ACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAG
GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC
GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCC
GACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT
CCGGGTAAA     (SEQ ID NO. 27)
```

cyno1-4 amino acid sequence

```
ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD
WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV
VEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK     (SEQ ID NO. 28)
```

FIG. 14

cynoKappa cDNA nucleotide sequence

CGCGCTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGAGGATCAGGTGAAATCTGGAACT
GTCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAGCGTAAAGTGGAAGGTGGAT
GGTGTCCTCAAAACGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAACACCTAC
AGCCTGAGCAGCACCCTGACGCTGAGCAGCACAGACTACCAGAGTCACAATGTCTATGCCTGCGAA
GTCACCCATCAGGGCCTGAGCTCGCCCGTCACCAAGAGCTTCAACAGAGGAGAGTGTTAGB
(SEQ ID NO. 29)

cynoKappa amino acid sequence

RAVAAPSVFIFPPSEDQVKSGTVSVVCLLNNFYPREASVKWKVDGVLKTGNSQESVTEQDSKDNTY
SLSSTLTLSSTDYQSHNVYACEVTHQGLSSPVTKSFNRGEC   (SEQ ID NO. 30)

FIG. 15

A. Nucleotide sequence alignments

```
                                                                                                                          _cyno33
                                                                                                                          _cyno35
                                                                                                                          _cyno36
                                                                                                                          _cyno477
                                                                                                                          _cyno32
```

```
        110       120       130       140       150       160       170       180       190       200
```

```
                                                                                                                          _cyno33
                                                                                                                          _cyno35
                                                                                                                          _cyno36
                                                                                                                          _cyno477
                                                                                                                          _cyno32
```

```
        210       220       230       240       250       260       270       280       290       300
```

```
                                                                                                                          _cyno33
                                                                                                                          _cyno35
                                                                                                                          _cyno36
                                                                                                                          _cyno477
                                                                                                                          _cyno32
```

```
        310       320       330       340       350       360       370       380       390       400
```

```
                                                                                                                          _cyno33
                                                                                                                          _cyno35
                                                                                                                          _cyno36
                                                                                                                          _cyno477
                                                                                                                          _cyno32
```

FIG. 16A

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```
          410       420       430       440       450       460       470       480       490       500
GGACCCCTGAGGTCACGTGCGTGGTGGTGTGGTGTAGACGTGAGCCAGGAAGAACCCGATGTCAACTGGTACGTGGACGGCGTGGAGGTTGCACAATGCCCA   _cyno33
GGACCCCTGAGGTCACGTGCGTGGTGGTGTGGTGTAGACGTGAGCCAGGAAGAACCCGATGTCAACTGGTACGTGGACGGCGTGGAGGTTGCACAATGCCCA   _cyno35
GGACCCCTGAGGTCACGTGCGTGGTGGTGTGGTGTAGACGTGAGCCAGGAAGAACCCGATGTCAACTGGTACGTGGACGGCGTGGAGGTTGCACAATGCCCA   _cyno36
GGACCCCTGAGGTCACGTGCGTGGTGGTGTGGTGTGGTGTGAGCCAGGAAGAAACCCGATGTCAACTGGTACGTGGACGGCGTGGAGGTTGCACAATGCCCA   _cyno477
GGACCCCTGAGGTCACGTGCGTGGTGGTGTGGTGTGGTGTGAGCCAGGAAGAAACCCGATGTCAAGTTCAAGTTCAAGTTGCACAATGCCCA            _cyno32
                                                                                  ****************
          510       520       530       540       550       560       570       580       590       600
GACGAAGCCACGGGAGGAGCAGTTCAACACAGCACGTACCGCGCGGTGGTCAGCGTCCTCACCGTCCTCCACCGTCCACACACCCAGGACTGGCTGAACGGCAAGGAGTACACGTGC   _cyno33
GACGAAGCCACGGGAGGAGCAGTTCAACACAGCACGTACCGCGCGGTGGTCAGCGTCCTCACCGTCCTGGTCAGCGTCCTCACCGTCCTGAACGGCAAGGAGTACACGTGC         _cyno35
GACGAAGCCACGGGAGGAGCAGTTCAACACAGCACGTACCGCGCGGTGGTCAGCGTCCTCACCGTCCTGGTCAGCGTCCTCACCGTCCTGAACGGCAAGGAGTACACGTGC         _cyno36
GACAAAGCCGCGGGAGGAGCAGTTCAACACAGCACGTATCCGCGGTGGTCAGCGTCCTCACCGTCCTCACCGTCCTGAACGGCAAGGAGTACACGTGC                     _cyno477
GACGAAGCCACGGGAGGAGCAGTTCAACACAGCACGTACCGCGCGGTGGTCAGCGTCCTCACCGTCCTGAACGGCAAGGAGTACACGTGC                             _cyno32
     ***** *****************************
          610       620       630       640       650       660       670       680       690       700
AAGGTCTCCAACAAAGCCCTCCCGGCCCCCGGCCCCCAAAGCCAGAGAAAACTGTCTCCAAAACCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCC   _cyno33
AAGGTCTCCAACAAAGCCCTCCCGGCCCCCGGCCCCCAAAGCCAGAGAAAACTGTCTCCAAAACCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCC   _cyno35
AAGGTCTCCAACAAAGCCCTCCCGGCCCCCGGCCCCCAAAGCCAGAGAAAACTGTCTCCAAAACCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCC   _cyno36
AAGGTCTCCAACAAAGCCCTCCCGGCCCCCGGCCCCCAAAGCCAGAGAAAACTGTCTCCAAAACCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCC   _cyno477
AAGGTCTCCAACAAAGGCCTCCCGGCCCCCATCTCCAAAGCCAGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACATCCTGCCCCCGCCCC   _cyno32
     *********** ******* *****       ********  *    *********************************** *** **********
          710       720       730       740       750       760       770       780       790       800
GGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTGGAGTGGGGCAGCAACGGGCAGCCGGA   _cyno33
GGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTGGAGTGGGGCAGCAACGGGCAGCCGGA   _cyno35
GGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGACCTGGTCAAAGGCTTCTACCCCAGCGACATCGTGGAGTGGGGCAGCAACGGGCAGCCGGA   _cyno36
GGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTGGAGTGGGGCAGCAACGGGCAGCCGGA   _cyno477
AGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCCAGCGACATCGTGGAGTGGGGCAGCAACGGGCAGCCGGA   _cyno32
 ****************************************************************** ***** *******************************
```

FIG. 16B

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```
              810        820        830        840        850        860        870        880        890        900
GAACACCTACAAGACCACACCCCGCCCGTGCTGGACTCCCTACTTCCTCTACAGCAAGCTCCTACAGCTTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC    _cyno33
GAACACCTACAAGACCACACCCCGCCCGTGCTGGACTCCCTACTTCCTCTACAGCAAGCTCCTACAGCTTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC    _cyno35
GAACACCTACAAGACCACACCCCGCCCGTGCTGGACTCCCTACTTCCTCTACAGCAAGCTCCTACAGCTTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC    _cyno36
GAACACCTACAAGAGAGACCACACCCCGCCCGTGCTGGACTCCCTACTTCCTCTACAGCAAGCTCCTACAGCTTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC    _cyno477
GAACACCTACAAGAGACCACACCCCGCCCGTGCTGGACTCCCTACTTCCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC    _cyno32
                **********  ****************


              910        920        930        940        950        960        970        980
ACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA---    _cyno33
ACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAAATGA    _cyno35
ACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAAATGA    _cyno36
ACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA    _cyno477
ACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA    _cyno32
                **********  ****************
```

B. Nucleotide sequence alignments

```
              110        120        130        140        150        160        170        180        190        200
GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCTCCAGGAGCACACGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC    _cyno4_2
GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCTCCAGGAGCACACGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC    _cyno4_2cys
GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCTCCAGGAGCACACGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC    _cyno2_4ds
---TCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCCTCCTCCAGGAGCACACGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC    _cyno686
GCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCCTCCTCCAGGAGCACACGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC    _cyno439
              *********  ****************        ****


              110        120        130        140        150        160        170        180        190        200
CCGAACCCGTGACTGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTCCAGTCCTACAGTCCTCACTCCCTCAGCAG    _cyno4_2
CCGAACCCGTGACTGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTCCAGTCCTACAGTCCTCACTCCCTCAGCAG    _cyno4_2cys
CCGAACCCGTGACCGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTCCAGTCCTACAGTCCTCACTCCCTCAGCAG    _cyno2_4ds
CCGAACCCGTGACCGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTCCAGTCCTACAGTCCTCACTCCCTCAGCAG    _cyno686
CCGAACCCGTGACCGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTCCAGTCCTACAGTCCTCACTCCCTCAGCAG    _cyno439
              *********  ****************        ****
```

FIG. 16C

```
              210       220       230       240       250       260       270       280       290       300
cyno2-4       CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAGCCCAGACCAAGGTGGACAAGACCAAGGTGGACAAGAGAGTTGAGTTC    _cyno4_2
_cyno2-4cys   CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAGCCCAGACCAAGGTGGACAAGACCAAGGTGGACAAGAGAGTTGAGTTC    _cyno4_2cys
_cynods1      CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAGCCCAGACCAAGACCAAGGTGGACAAGAGAGTTGAGTTC            _cyno2_4ds
_cyno686      CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAGCCCAGACCAAGGTGGACAAGACCAAGGTGGACAAGAGAGTTGAGTTC    _cyno686
_cyno439      CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAGCCCAGACCAAGGTGGACAAGACCAAGGTGGACAAGAGAGTTGAGTTC    _cyno439
              ********************************* ************ ******************************    *********************

              310       320       330       340       350       360       370       380       390       400
cyno2-4       ACAC--------------CCCCATGCCCACCATGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG                      _cyno4_2
_cyno2-4cys   ACAC--------------CCCCATGCCCACCATGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG                      _cyno4_2cys
_cynods1      ACAC--------------CCCCATGCCCACCATGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG                      _cyno2_4ds
_cyno686      ACACGCCCCATGTGATGACAACTCCCCCATGCCCACCATGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG               _cyno686
_cyno439      ACACGCCCCATGTGATGACAACTCCCCCATGCCCACCATGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG               _cyno439
              ****                       ************************************************************************

              410       420       430       440       450       460       470       480       490       500
cyno2-4       ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGT         _cyno4_2
_cyno2-4cys   ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGT         _cyno4_2cys
_cynods1      ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGT         _cyno2_4ds
_cyno686      ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGT         _cyno686
_cyno439      ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGT         _cyno439
              *****************************************************************************************************

              510       520       530       540       550       560       570       580       590       600
cyno2-4       GGAGGTGCATAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGCGTCGTCAGCGTCCTCACCGTCACACACCAGGACTGGCTGAAC           _cyno4_2
_cyno2-4cys   GGAGGTGCATCATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCAACAGCACGTTCCGCGTCCTCACCGTCACACACCAGGACTGGCTGAAC         _cyno4_2cys
_cynods1      GGAGGTGCATCATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGGTCAACAGCACGTTCCGCGTCCTCACCGTCACACACCAGGACTGGCTGAAC         _cyno2_4ds
_cyno686      GGAGGTGCATCATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGCGTCCTCACCGTCGTGTGCACCGTCACACACCAGGACTGGCTGAAC         _cyno686
_cyno439      GGAGGTGCACAATGCCCAGACGAAGCCGCGGGAGGAGCAGTTCAACAGCACATATCGTGTGTGCACCGTCGTGTGCACCGTCACACACCAGGACTGGCTGAAC         _cyno439
              *********  *************** * ************************     **  **   *********** ** *********************
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FIG. 16D

20/30

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           610       620       630       640       650       660       670       680       690       700
cyno2-4     GGCAAGGAGTACACGTGCAAGGTCTCCAACAAACCATCTCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAGCCGCAGGTGT    cyno4_2
cyno2-4cys  GGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGCCTCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAGCCGCAGGTGT    cyno4_2cys
cynods1     GGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGCCTCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAGCCGCAGGTGT    cyno2_4ds
cyno686     GGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGCCCCGGCCCCCCGGCCCCATCGAGAGAAACCATCTCCAAAGACAAAGGGCAGCCCGAGAGAGCTCAGGTGT    cyno686
cyno439     GGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGCCTCCGGCCCCCATCGAGAGAAACCATCTCCAAAGACAAAGGGCAGCCCGAGAGAGCTCAGGTGT    cyno439
            ********* *** **************************** ***** * * *** *** ***** ****************** *******

           710       720       730       740       750       760       770       780       790       800
cyno2-4     ACATCCTGCCCCCGCCCCGCCCCCAGGAGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGA    cyno4_2
cyno2-4cys  ACATCCTGCCCCCGCCCCGCCCCCAGGAGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGA    cyno4_2cys
cynods1     ACATCCTGCCCCCGCCCCGCCCCCAGGAGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGA    cyno2_4ds
cyno686     ACACCCTGCCCCCGTCCCGGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGA    cyno686
cyno439     ACACCCTGCCCCCGTCCCGGGAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGA    cyno439
            ***     ************************* *************************************** ******************

           810       820       830       840       850       860       870       880       890       900
cyno2-4     GAGCAACGGGCAGCCGGAGAACAACTACAAGACCACACCCCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCATCGTGGACAAGAGAGC    cyno4_2
cyno2-4cys  GAGCAACGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCATCGTGGACAAGAGAGC    cyno4_2cys
cynods1     GAGCAACGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCATCGTGGACAAGAGAGC    cyno2_4ds
cyno686     GAGCAGCGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGAGC    cyno686
cyno439     GAGCAGCGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGAGC    cyno439
            ***** ******************************** ********************************************** ****************

           910       920       930       940       950       960       970       980       990
cyno2-4     AGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA    cyno4_2
cyno2-4cys  AGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA    cyno4_2cys
cynods1     AGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA---    cyno2_4ds
cyno686     AGGTGGCAGCAGCGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA    cyno686
cyno439     AGGTGGCAGCAGCGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA    cyno439
            ************ ****** ********************************************************************* ********
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FIG. 16E

C. Nucleotide sequence alignments

```
                    10        20        30        40        50        60        70        80        90       100
_cyno3_18  GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACAGCAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC  _cyno3_18
_cyno3_16  GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACAGCAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC  _cyno3_16
_cyno1_3   GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACAGCAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC  _cyno1_3
_cyno1_4   GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACAGCAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC  _cyno1_4
           ********************************************************************************************************

                   110       120       130       140       150       160       170       180       190       200
_cyno3_18  CTGAACCCGTGACCGTGTCGTGGAACTCAGGCTCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGCAG  _cyno3_18
_cyno3_16  CTGAACCCGTGACCGTGTCGTGGAACTCAGGCTCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGCAG  _cyno3_16
_cyno1_3   CTGAACCCGTGACCGTGTCGTGGAACTCAGGCTCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGCAG  _cyno1_3
_cyno1_4   CTGAACCCGTGACCGTGTCGTGGAACTCAGGCTCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGCAG  _cyno1_4
           **************************************************************************************************

                   210       220       230       240       250       260       270       280       290       300
_cyno3_18  CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATA  _cyno3_18
_cyno3_16  CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATA  _cyno3_16
_cyno1_3   CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATA  _cyno1_3
_cyno1_4   CGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATA  _cyno1_4
           **************************************************************************************************

                   310       320       330       340       350       360       370       380       390       400
_cyno3_18  ---ACATGTGGTGGCAGCAAACCTCCCACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCA  _cyno3_18
_cyno3_16  AAAACATGTGGTGGCAGCAAACCTCCCACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCA  _cyno3_16
_cyno1_3   AAAACATGTGGTGGCAGCAAACCTCCCACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCA  _cyno1_3
_cyno1_4   AAAACATGTGGTGGCAGCAAACCTCCCACGTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCA  _cyno1_4
           ************************************************************************************************
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FIG. 16F

22/30

FIG. 16G

FIG. 16H

AA sequence alignment

```
                10        20        30        40        50        60        70        80        90       100
_cyno2_4    ASTKGPSVFPLASSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEF    _cyno2_4
_cyno2_4cys ASTKGPSVFPLASCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEF    _cyno2_4cys
_cynods1    ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEF    _cyno2_4ds
_cyno33     ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKIVGL    _cyno33
_cyno35     ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKIVGL    _cyno35
_cyno36     ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGL    _cyno36
_cyno477    -STKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGL    _cyno477
_cyno32     ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEF    _cyno32
_cyno686    -STKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEF    _cyno686
_cyno439    ASTKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEF    _cyno439
_cyno1_4    ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEI    _cyno1_4
_cyno1_3    ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEI    _cyno1_3
_cyno3_18   ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGSLTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEI    _cyno3_18
_cyno3_16   ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGSLTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEI _cyno3_16
            ********** *****.:******* *******************************************************************:*:*****  *
```

```
               110       120       130       140       150       160       170       180       190       200
_cyno2_4    ------TPPCPPCPAP--ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPREROFNSTYRVVSVLTVTHQDWL    _cyno2_4
_cyno2_4cys ------TPPCPPCPAP--ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPREROFNSTYRVVSVLTVTHQDWL    _cyno2_4cys
_cynods1    ------TPPCPPCPAP--ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPREROFNSTYRVVSVLTVTHQDWL    _cyno2_4ds
_cyno33     ------PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL    _cyno33
_cyno35     ------PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL    _cyno35
_cyno36     ------PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL    _cyno36
_cyno477    ------PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL    _cyno477
_cyno32     ------PCRSTCPPCPA-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWL    _cyno32
_cyno686    ---TRPCDDTTPPCPPCPAPELLGGPSVFVFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGAEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWL _cyno686
_cyno439    ---TRPCDDTTPPCPPCPAPELLGGPSVFVFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAQTKPRERQFNSTYRVVSVLTVTHQDWL _cyno439
_cyno1_4    KTCGGGSKPPTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL   _cyno1_4
_cyno1_3    KTCGGGSKPPTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL   _cyno1_3
_cyno3_18   -TCGGGSKPPTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDDEVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL   _cyno3_18
_cyno3_16   KTCGGGSKPPTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDDEVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDWL   _cyno3_16
            *.*  ::*********:..*:*.::*********************************:.****:****.****:****::******************
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FIG. 17A

```
                  210        220        230        240        250        260        270        280        290        300

_cyno2_4          NGKEYTCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  _cyno2_4
cyno2_4cys        NGKEYTCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  cyno2_4cys
_cynods1          NGKEYTCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  _cyno2_4ds
_cyno33           NGKEYTCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  _cyno33
_cyno35           NGKEYTCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  _cyno35
_cyno36           NGKEYTCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWASNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  _cyno36
_cyno477          NGKEYTCKVSNKALPAPRQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLIKGFYPSDIVVEWASNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  _cyno477
_cyno32           NGKEYTCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQPENTYKTTPPVLDSDGSYFLYSKLTVDK  _cyno32
_cyno686          NGKEYTCKVSNKALPAPIQKTISDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK   _cyno686
_cyno439          NGKEYTCKVSNKALPAPIQKTISDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK   _cyno439
_cyno1_4          NGKEYTCKVSNKALPAPIQKTISDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK   _cyno1_4
_cyno1_3          NGKEYTCKVSNKALPAPIQKTISDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK   _cyno1_3
_cyno3_18         NGKEYTCKVSNKALPAPIQKTISDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK   _cyno3_18
_cyno3_16         NGKEYTCKVSNKALPAPIQKTISDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVVEWESSGQPENTYKTTPPVLDSDGSYFLYSKLTVDK   _cyno3_16
                  ***********:****  :**:** *********  *** .**.*****.***:**** . ********. *** *.********************  ***


                  310        320        330

_cyno2_4          SRWQQGNTFSCSVMHEALLHNHYTQKSLSVSPGK  _cyno2_4
cyno2_4cys        SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK   cyno2_4cys
_cynods1          SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK   _cyno2_4ds
_cyno33           SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK   _cyno33
_cyno35           SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK   _cyno35
_cyno36           SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK   _cyno36
_cyno477          SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK   _cyno477
_cyno32           SRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK   _cyno32
_cyno686          SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   _cyno686
_cyno439          SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   _cyno439
_cyno1_4          SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   _cyno1_4
_cyno1_3          SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   _cyno1_3
_cyno3_18         SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   _cyno3_18
_cyno3_16         SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   _cyno3_16
                  *******.*********.*****************:****
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FIG. 17B

A. Heavy Chain Variable Region Nucleotide Sequences

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                                              FR1
H1    1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H2    1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H3    1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H4    1   GAGGTTCAGT TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H5    1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H6    1   GAGGTTCAGT TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H7    1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H8    1   GAGGTTCAGT TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H9    1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H10   1   GAGGTTCAGT TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H11   1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H12   1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H13   1   GAGGTTCAGC TGGTGCAGTC TGGGGGAGGC TTGGTACATC CTGGGGGGTC CCTGAGACTC   60
H14   1   GAGGTTCAGT TGGTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGAGACTC   60

                                              CDR1
H1    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H2    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H3    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H4    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H5    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H6    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H7    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H8    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H9    61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H10   61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H11   61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H12   61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H13   61  TCCTGTGCAG GCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120
H14   61  TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGAAATGCTA TGTTCTGGGT TCGCCAGGCT   120

                FR2                                    CDR2
H1    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAACTATGCA   180
H2    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
H3    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
H4    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAACTATGCA   180
H5    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAACTATGCA   180
H6    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAACTATGCA   180
H7    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
H8    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAACTATGCA   180
H9    121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
H10   121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAACTATGCA   180
H11   121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
H12   121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
H13   121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
H14   121 CCAGGAAAAG GTCTGGAGTG GGTATCAGGT ATTGGTACTG GTGGTGCCAC AAGCTATGCA   180
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FIG. 18A

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                                                        FR3
H1    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H2    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H3    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H4    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H5    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H6    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H7    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H8    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H9    181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H10   181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H11   181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H12   181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H13   181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240
H14   181 GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATG CCAAGAACTC CTTGTATCTT  240


H1    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H2    241 CAAATGAACA GCCTGAGTGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H3    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H4    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H5    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H6    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H7    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H8    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H9    241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H10   241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H11   241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H12   241 CAAATGAACA GCCTGAGAGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H13   241 CAAATGAACA GCCTGAGTGC CGAGGACATG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300
H14   241 CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCAAG AGGGAGGTAC  300


          CDR3                    FR4
H1    301 TACTTTGACT ACTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:47)
H2    301 TACTTCACCC ACTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:48)
H3    301 TGGTACAACA ACTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:49)
H4    301 TACTTCCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:50)
H5    301 TACTTCACGA GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:51)
H6    301 TGGTACCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:52)
H7    301 TGGTACCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:53)
H8    301 TGGTTCCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:54)
H9    301 TGGTTCCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:55)
H10   301 TGGTACCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:56)
H11   301 TGGTACCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:57)
H12   301 TACTTCCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:58)
H13   301 TACTTCCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:59)
H14   301 TACTTCCCGT GGTGGGGCCA GGGAACCCTG GTCACCGTCT CCTCA  345  (SEQ ID NO:60)
```

FIG. 18B

B. Heavy Chain Variable Region Amino Acid Sequences

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
H1	EVQLVQSGGGLVHPGGSLRLSCAGSGFTF	SRNAMF	WVRQAPGKGLEWVS	GIGTGGATNYADSVKG	RFTISRDNAKNSLYLQMNSLRAEDMAVYYCARGR	YYFDY	WGQGTLVTVS
H2	---------------------------	------	-------------	----------------	-----------------S----------------	--TH-	----------
H3	---------------------------	------	-------------	------S---------	----------------------------------	WYNN-	----------
H4	---------------------------	------	-------------	----------------	----------------------------------	-PW--	----------
H5	---------------------------	------	-------------	----------------	----------------------------------	-TR--	----------
H6	---------------------------	------	-------------	----------------	----------------------------------	-YPW-	----------
H7	---------------------------	------	-------------	------S---------	----------------------------------	-YPW-	----------
H8	---------------------------	------	-------------	----------------	----------------------------------	W-PW-	----------
H9	---------------------------	------	-------------	------S---------	----------------------------------	W-PW-	----------
H10	---------------------------	------	-------------	------S---------	----------------------------------	WYPW-	----------
H11	---------------------------	------	-------------	------S---------	----------------------------------	WYPW-	----------
H12	---------------------------	------	-------------	----------------	----------------------------------	-PW--	----------
13	-------------------------A-	------	-------------	------S---------	----------------S-----------------	-PW--	----------
14	-E------Q------------------	------	-------------	----------------	--------------T-------------------	-PW--	----------

H1 = (SEQ ID NO:61)
H2 = (SEQ ID NO:62)
H3 = (SEQ ID NO:63)
H4 = (SEQ ID NO:64)
H5 = (SEQ ID NO:65)
H6 = (SEQ ID NO:66)
H7 = (SEQ ID NO:67)
H8 = (SEQ ID NO:68)
H9 = (SEQ ID NO:69)
H10 = (SEQ ID NO:70)
H11 = (SEQ ID NO:71)
H12 = (SEQ ID NO:72)
H13 = (SEQ ID NO:73)
H14 = (SEQ ID NO:74)

FIG. 18C

A. Light Chain Variable Region Nucleotide Sequences

```
L1  1  GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60
L2  1  GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCGGGGGA AAGAGCCACC  60
L3  1  GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCGGGGGA AAGAGCCACC  60
L4  1  GAAATTGTGA TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60
L5  1  GATATTGTGC TGACCCAGTC TCCAGCCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60
L6  1  GATATTGTGC TGACGCAGAC TCCAGCCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60

                    CDR1
L1 61  CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AGCAGCTACT TAGCCTGGTA CCAGCAGAAA  120
L2 61  CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AACAGCTACT TAGCCTGGTA CCAGCAGAAA  120
L3 61  CTCTCCTGCA GGGCCAGTCA GACTGTTAAC AGCGACTACT TAGCCTGGTA CCAGCAGAAA  120
L4 61  CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AGCGACTACT TAGCCTGGTA CCAGCAGAAA  120
L5 61  CTCTCCTGCA GGGCCAGTCA GAGTGTTAAC AGCAACTACT TAGCCTGGTA CCAGCAGAAA  120
L6 61  CTCTCCTGCA GGGCCAGTCA GAGTGTTGGC AGCAGCTACT TAGCCTGGTA CCAGCAGAGA  120

            FR2                              CDR2
L1 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTTT GGTGCATCCA GCAGGGCCAC TGGCATCCCA  180
L2 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCCA GCAGGGCCCC TGGCATCCCA  180
L3 121 CCGGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCA  180
L4 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCTA GCAGGGCCTC TGGCATCCCA  180
L5 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTACATCCT ACAGGGCCAC TGGCATCCCA  180
L6 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCG  180

                    FR3
L1 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L2 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L3 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L4 181 GACAGGTTCA GTGGCAGTGG GTTTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L5 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAC CAGACTGGAG  240
L6 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACGATCAG CAGACTGGAG  240

                                            CDR3
L1 241 CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGGTA GCTCACCTCC GTGGACGTTC  300
L2 241 CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGATC ACTCAGCAGG GTGGACGTTC  300
L3 241 CCTGAAGATT TTGCAGTCTA TTACTGTCAG CAGTATGGTA GGTCACCTCC GTGGACGTTC  300
L4 241 CCTGAAGATT TTGCAATATA TTACTGTCAG CAGTATGGTA GCTCACCTCC GTGGACGTTC  300
L5 241 CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGGTA GCTCACCACC GTGGACGTTC  300
L6 241 CCTGAAGATT TTGCAGTGTA TTATTGTCAG CAGTATGGAA GTTCACCTCC GTGGATGTTC  300

            FR4
L1 301 GGCCAAGGGA CCAAGGTGGA AATCAAA  327 (SEQ ID NO:75)
L2 301 GGCCAAGGGA CCAAGGTGGA GATCAAA  327 (SEQ ID NO:76)
L3 301 GGCCAAGGGA CCAAAGTGGA TATCAAA  327 (SEQ ID NO:77)
L4 301 GGCCAAGGGA CCAAGGTGGA AATCAAA  327 (SEQ ID NO:78)
L5 301 GGCCAAGGGA CACGACTGGA GATTAAA  327 (SEQ ID NO:79)
L6 301 GGCCAAGGGA CCAAGGTGGA GATCAAA  327 (SEQ ID NO:80)
```

FIG. 19A

B. Light Chain Variable Region Amino Acid Sequences

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
L1	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIF	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPPWTF	GQGTKVEIK
L2	---------------------	---------N--	--------------	Y------	-------------------------------	--DH-AG---	--------
L3	---------------------	--T-N-D-----	--------------	Y------	-------------------------------	--R-------	-------D
L4	-----M---------------	--------D----	--------------	Y-----S	--------------F----------------	----------	--------
L5	D-----A--------------	--N-N-------	--------------	Y-T-Y--	------T-I--------------------	----------	-----RL-
L6	D-----T-A------------	--G---------	----R---------	-------	-------------------------------	--M-------	--------

L1 = (SEQ ID NO:81)
L2 = (SEQ ID NO:82)
L3 = (SEQ ID NO:83)
L4 = (SEQ ID NO:84)
L5 = (SEQ ID NO:85)
L6 = (SEQ ID NO:86)

FIG. 19B